

RAW SEQUENCE LISTING

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Application Serial Number: 10/538, 544
Source: PCT
Date Processed by STIC: 06/21/2005

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PCT

RAW SEQUENCE LISTING

DATE: 06/21/2005

PATENT APPLICATION: US/10/538,544

TIME: 13:45:59

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06172005\J538544.raw

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3 <110> APPLICANT: BASF Aktiengesellschaft
7 <120> TITLE OF INVENTION: Malate dehydrogenase as target for herbicides
11 <130> FILE REFERENCE: PF 0000 054200
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/538,544
C--> 15 <141> CURRENT FILING DATE: 2005-06-10
15 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
25 <211> LENGTH: 673
27 <212> TYPE: DNA
29 <213> ORGANISM: Nicotiana tabacum
33 <400> SEQUENCE: 1
34 gcggccgcta aacctccttg ttctttttacg ccagaggaag ctgaatatatt aacatctcgt      60
36 atacaaaatg ggggaactga agttgttgag gcaaaagctg gtgctgggtc ggcaactctc      120
38 tctatggcat atgctgcggt taaatttgcc gacgcatggt tgcattggatt gagaggagat      180
40 gctggcattg tagaatgtgc ctttgtgtct tctcaggtga ctgaacttcc attttttcgca      240
42 tcaaaagtat ggcttgccg caacggaggt gaagaaatat accccttggt tccctaaat      300
44 gaatacgaga ggtctgggct tgagaaggca aggaaagagt tggcaacaag tgttcagaag      360
46 ggtgtcaact ttgtaaagaa atgagcagac agctacatga cttccaaaag atgcttttat      420
48 gtgggctata tatctcaaat ccgcagttcc agaaaataag agtagtttct ttcttgtatt      480
50 aaagggcaaa tcctgttcta attttctata gattgatgcc ttggtgcaga aaataaatgt      540
52 actatttggt catctaaaat aacaacagtc cccagtgcatt gttggacttg caaagtatta      600
54 catcctttga agcaagggtc tgttatggac tttttgacag tatggatatt taaagggtc      660
56 ggagagcggc cgc                                          673
59 <210> SEQ ID NO: 2
61 <211> LENGTH: 1505
63 <212> TYPE: DNA
65 <213> ORGANISM: Nicotiana tabacum
69 <220> FEATURE:
71 <221> NAME/KEY: CDS
73 <222> LOCATION: (148)..(1221)
75 <223> OTHER INFORMATION:
W--> 79 <400> 2
80 ctaatacgac tcactatagg gcaagcagtg gtatcaacgc agagtacgcg ggggggaaac      60
82 aaaattcaat tacttacctt gatttctact acctctcttt ctcatcataa ttcaaacaca      120
84 caaattctca agcccaagtc ttagaat atg cag aac ggt gca gag acc tat cga      174
85                               Met Gln Asn Gly Ala Glu Thr Tyr Arg
86                               1                               5
88 cga atg gcc acc atc tca gct cac ctt aac ccc tct cct tct tct cat      222
89 Arg Met Ala Thr Ile Ser Ala His Leu Asn Pro Ser Pro Ser Ser His
90 10                               15                               20                               25
92 cag atg gag gga ggt gtg ggt ttg agc cga gct aat tgc agg gcg aaa      270
93 Gln Met Glu Gly Gly Val Gly Leu Ser Arg Ala Asn Cys Arg Ala Lys

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94	30	35	40	
96	ggg ggt tct cca gga ttc aaa gtc gcg atc ttg ggt gct gca gga ggt	318		
97	Gly Gly Ser Pro Gly Phe Lys Val Ala Ile Leu Gly Ala Ala Gly Gly			
98	45	50	55	
100	att ggt cag cca ctt gct atg ctt atg aaa acg aat cca ctg gtt tca	366		
101	Ile Gly Gln Pro Leu Ala Met Leu Met Lys Thr Asn Pro Leu Val Ser			
102	60	65	70	
104	gtt ctg cat ctt tat gat gtt gcc aat act cct ggt gta act gct gac	414		
105	Val Leu His Leu Tyr Asp Val Ala Asn Thr Pro Gly Val Thr Ala Asp			
106	75	80	85	
108	att agc cac atg gac act ggt gcc gtg gta cgt ggt ttt cta ggg cct	462		
109	Ile Ser His Met Asp Thr Gly Ala Val Val Arg Gly Phe Leu Gly Pro			
110	90	95	100	105
112	caa caa ttg gaa gat gct ctc act ggc atg gac ctt gta ata atc cct	510		
113	Gln Gln Leu Glu Asp Ala Leu Thr Gly Met Asp Leu Val Ile Ile Pro			
114	110	115	120	
116	gct ggt gtt cct aga aaa cca ggc atg aca aga gat gat ctt ttc aac	558		
117	Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn			
118	125	130	135	
120	atc aat gca gga att gtg agg act tta tgt gaa gga att gcc aag tgc	606		
121	Ile Asn Ala Gly Ile Val Arg Thr Leu Cys Glu Gly Ile Ala Lys Cys			
122	140	145	150	
124	tgt cct aag gcc att gtt aac ata att agt aat cct gtt aac tct aca	654		
125	Cys Pro Lys Ala Ile Val Asn Ile Ile Ser Asn Pro Val Asn Ser Thr			
126	155	160	165	
128	gta cca att gct gca gag gtt ttc aag aag gct ggc acc ttt gat ccg	702		
129	Val Pro Ile Ala Ala Glu Val Phe Lys Lys Ala Gly Thr Phe Asp Pro			
130	170	175	180	185
132	agg aga ctg ttg ggc gtg aca atg ctt gat att gtc aga gcc aat aca	750		
133	Arg Arg Leu Leu Gly Val Thr Met Leu Asp Ile Val Arg Ala Asn Thr			
134	190	195	200	
136	ttt gtg gct gaa gtt ttg ggg ctt gat cct agg gaa gtg gat gtt cca	798		
137	Phe Val Ala Glu Val Leu Gly Leu Asp Pro Arg Glu Val Asp Val Pro			
138	205	210	215	
140	gtt gtg ggg ggt cat gct ggc gtt aca att cta cct ctt tcc cag	846		
141	Val Val Gly Gly His Ala Gly Val Thr Ile Leu Pro Leu Leu Ser Gln			
142	220	225	230	
144	gtt aaa cct cct tgt tct ttt acg cca gag gaa act gaa tat tta aca	894		
145	Val Lys Pro Pro Cys Ser Phe Thr Pro Glu Glu Thr Glu Tyr Leu Thr			
146	235	240	245	
148	tct cgt ata caa aat ggg gga act gaa gtt gtt gag gca aaa gct ggt	942		
149	Ser Arg Ile Gln Asn Gly Gly Thr Glu Val Val Glu Ala Lys Ala Gly			
150	250	255	260	265
152	gct ggt tcg gca act ctc tct atg gca tat gct gcg gtt aaa ttt gcc	990		
153	Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Ala Val Lys Phe Ala			
154	270	275	280	
156	gac gca tgt ttg cat gga ttg aga gga gat gct ggc att gta gaa tgt	1038		
157	Asp Ala Cys Leu His Gly Leu Arg Gly Asp Ala Gly Ile Val Glu Cys			
158	285	290	295	

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160 gcc ttt gtg tct tct cag gtg act gaa ctt cca ttt ttc gca tca aaa      1086
161 Ala Phe Val Ser Ser Gln Val Thr Glu Leu Pro Phe Phe Ala Ser Lys
162          300                      305                      310
164 gta cgg ctt ggc cgc aac gga gtt gaa gaa ata tac ccc ctt ggt ccc      1134
165 Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Tyr Pro Leu Gly Pro
166          315                      320                      325
168 cta aat gaa tac gag agg tct ggg ctt gag aag gca aag aaa gag ctg      1182
169 Leu Asn Glu Tyr Glu Arg Ser Gly Leu Glu Lys Ala Lys Lys Glu Leu
170 330          335                      340                      345
172 gca aca agt gtt cag aag ggt gtc aac ttt gta aag aaa tgagcagaca      1231
173 Ala Thr Ser Val Gln Lys Gly Val Asn Phe Val Lys Lys
174          350                      355
176 gctacatgac ttccaaaaga tgcttttatg tgggctatat atctcaaadc cgcagttcca      1291
178 gaaaataaga gtagtttctt tcttgattata aagggcaaat cctgttctaa ttttctatag      1351
180 attgatgcct tgggtgcagaa aataaatgta ctatttggtc atctaaaata acaacagtcc      1411
182 ccagtgcattg ttggacttgc aaagtattac atcctttgaa gcaagggctt gttatggact      1471
184 ttttgacagt atggatattt aaagggcttg gaga                                1505
187 <210> SEQ ID NO: 3
189 <211> LENGTH: 358
191 <212> TYPE: PRT
193 <213> ORGANISM: Nicotiana tabacum
197 <400> SEQUENCE: 3
199 Met Gln Asn Gly Ala Glu Thr Tyr Arg Arg Met Ala Thr Ile Ser Ala
200 1          5          10          15
203 His Leu Asn Pro Ser Pro Ser Ser His Gln Met Glu Gly Gly Val Gly
204          20          25          30
207 Leu Ser Arg Ala Asn Cys Arg Ala Lys Gly Gly Ser Pro Gly Phe Lys
208          35          40          45
211 Val Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Met
212          50          55          60
215 Leu Met Lys Thr Asn Pro Leu Val Ser Val Leu His Leu Tyr Asp Val
216 65          70          75          80
219 Ala Asn Thr Pro Gly Val Thr Ala Asp Ile Ser His Met Asp Thr Gly
220          85          90          95
223 Ala Val Val Arg Gly Phe Leu Gly Pro Gln Gln Leu Glu Asp Ala Leu
224          100         105         110
227 Thr Gly Met Asp Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro
228          115         120         125
231 Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Arg
232          130         135         140
235 Thr Leu Cys Glu Gly Ile Ala Lys Cys Cys Pro Lys Ala Ile Val Asn
236 145          150         155         160
239 Ile Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val
240          165         170         175
243 Phe Lys Lys Ala Gly Thr Phe Asp Pro Arg Arg Leu Leu Gly Val Thr
244          180         185         190
247 Met Leu Asp Ile Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly
248          195         200         205
251 Leu Asp Pro Arg Glu Val Asp Val Pro Val Val Gly Gly His Ala Gly

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252      210      215      220
255 Val Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro Pro Cys Ser Phe
256 225      230      235      240
259 Thr Pro Glu Glu Thr Glu Tyr Leu Thr Ser Arg Ile Gln Asn Gly Gly
260      245      250      255
263 Thr Glu Val Val Glu Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Ser
264      260      265      270
267 Met Ala Tyr Ala Ala Val Lys Phe Ala Asp Ala Cys Leu His Gly Leu
268      275      280      285
271 Arg Gly Asp Ala Gly Ile Val Glu Cys Ala Phe Val Ser Ser Gln Val
272      290      295      300
275 Thr Glu Leu Pro Phe Phe Ala Ser Lys Val Arg Leu Gly Arg Asn Gly
276 305      310      315      320
279 Val Glu Glu Ile Tyr Pro Leu Gly Pro Leu Asn Glu Tyr Glu Arg Ser
280      325      330      335
283 Gly Leu Glu Lys Ala Lys Lys Glu Leu Ala Thr Ser Val Gln Lys Gly
284      340      345      350
287 Val Asn Phe Val Lys Lys
288      355

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291 <210> SEQ ID NO: 4

293 <211> LENGTH: 16

295 <212> TYPE: DNA

297 <213> ORGANISM: Artificial Sequence

301 <220> FEATURE:

303 <223> OTHER INFORMATION: Primer

305 <400> SEQUENCE: 4

306 agaattcgcg gccgct

16

309 <210> SEQ ID NO: 5

311 <211> LENGTH: 32

313 <212> TYPE: DNA

315 <213> ORGANISM: Artificial Sequence

319 <220> FEATURE:

321 <223> OTHER INFORMATION: Primer

323 <400> SEQUENCE: 5

324 ctcattgcggc cgcgcgcaac gcaattaatg tg

32

327 <210> SEQ ID NO: 6

329 <211> LENGTH: 32

331 <212> TYPE: DNA

333 <213> ORGANISM: Artificial Sequence

337 <220> FEATURE:

339 <223> OTHER INFORMATION: Primer

341 <400> SEQUENCE: 6

342 tcatgcggcc gcgagatcca gttcgatgta ac

32

345 <210> SEQ ID NO: 7

347 <211> LENGTH: 21

349 <212> TYPE: DNA

351 <213> ORGANISM: Artificial Sequence

355 <220> FEATURE:

357 <223> OTHER INFORMATION: Primer

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Output Set: N:\CRF4\06172005\J538544.raw

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359 <400> SEQUENCE: 7
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363 <210> SEQ ID NO: 8
365 <211> LENGTH: 21
367 <212> TYPE: DNA
369 <213> ORGANISM: Artificial Sequence
373 <220> FEATURE:
375 <223> OTHER INFORMATION: Primer
377 <400> SEQUENCE: 8
378 gtaaggatct gagctacaca t 21
381 <210> SEQ ID NO: 9
383 <211> LENGTH: 17
385 <212> TYPE: DNA
387 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:
393 <223> OTHER INFORMATION: Primer
395 <400> SEQUENCE: 9
396 atgagggcga aaggggg 17
399 <210> SEQ ID NO: 10
401 <211> LENGTH: 25
403 <212> TYPE: DNA
405 <213> ORGANISM: Artificial Sequence
409 <220> FEATURE:
411 <223> OTHER INFORMATION: Primer
413 <400> SEQUENCE: 10
414 tttctttaca aagttgacac ccttc 25
417 <210> SEQ ID NO: 11
419 <211> LENGTH: 17
421 <212> TYPE: DNA
423 <213> ORGANISM: Artificial Sequence
427 <220> FEATURE:
429 <223> OTHER INFORMATION: Primer
431 <400> SEQUENCE: 11
432 atgcgggcaa aaggtgg 17
435 <210> SEQ ID NO: 12
437 <211> LENGTH: 21
439 <212> TYPE: DNA
441 <213> ORGANISM: Artificial Sequence
445 <220> FEATURE:
447 <223> OTHER INFORMATION: Primer
449 <400> SEQUENCE: 12
450 tttcttcgca aagtaacac c 21

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/538,544

DATE: 06/21/2005

TIME: 13:46:00

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06172005\J538544.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:75